

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: HUSE, WILLIAM D.
- (ii) TITLE OF INVENTION: SURFACE EXPRESSION LIBRARIES OF HETEROMERIC RECEPTORS
- (iii) NUMBER OF SEQUENCES: 75
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
 - (B) STREET: 444 SO. FLOWER STREET, SUITE 200
 - (C) CITY: LOS ANGELES
 - (D) STATE: CALIFORNIA
 - (E) COUNTRY: UNITED STATES
 - (F) ZIP: 90071
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: CAMPBELL, CATHRYN A.
 - (B) REGISTRATION NUMBER: 31,815
 - (C) REFERENCE/DOCKET NUMBER: P31 8882
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 619-535-9001
 - (B) TELEFAX: 619-535-8949

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7445 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: circular

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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TTGGAGTTTG CTTCCGGTCT GGTTCGCTTT GAAGTCCGAA TTAAAACGCG ATATTTGAAG	360
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GGTTTTATC GTCGTCTGGT AAACGAGGGT TATGATAGTG TTGCTCTTAC TATGCCTCGT	660
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TGAGTACAAT GGCTACGCTT GGGCTATGGT AGTAGTTATA GTTGGTGCTA CCATAGGGAT	6540

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GCTCTGAGGC TTTATTGCTT AATTTTGCTA ATTCTTTGCC TTGCCTGTAT GATTATTGG	7440
ACGTT	7445

(2) INFORMATION FOR SEQ ID NO:2:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 7317 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: circular

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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TAGTGCACCT AAAGATATTT TAGATAACCT TCCTCAATTC CTTTCTACTG TTGATTGCGC	4800

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TCTGGATATT ACCAGCAAGG CCGATAGTTT GAGTTCTTCT ACTCAGGCAA GTGATGTTAT	5280
TACTAATCAA AGAAGTATTG CTACAACGGT TAATTTGCGT GATGGACAGA CTCTTTTACT	5340
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ATTTGGGTGA TGGTTCACGT AGTGGGGCCAT CGCCCTGATA GACGGTTTTT CGCCCTTTGA	5760
CGTTGGAGTC CACGTTCTTT AATAGTGGAC TCTTGTCCA AACTGGAACA ACACTCAACC	5820
CTATCTCGGG CTATTCTTTT GATTTATAAG GGATTTTGCC GATTTGCGAA CCACCATCAA	5880
ACAGGATTTT CGCCTGCTGG GGCAAACCAG CGTGGACCGC TTGCTGCAAC TCTCTCAGGG	5940
CCAGGCGGTG AAGGGCAATC AGCTGTTGCC CGTCTCGCTG GTGAAAAGAA AAACCACCTT	6000
GGCGCCCAAT ACGCAAACCG CCTCTCCCCG CGCGTTGGCC GATTCATTAA TGCAGCTGGC	6060
ACGACAGGTT TCCCGACTGG AAAGCGGGCA GTGAGCGCAA CGCAATTAAT GTGAGTTAGC	6120
TCACTCATTG GGCACCCAG GCTTTACACT TTATGCTTCC GGCTCGTATG TTGTGTGGAA	6180
TTGTGAGCGG ATAACAATTT CACACGCCAA GGAGACAGTC ATAATGAAAT ACCTATTGCC	6240
TACGGCAGCC GCTGGATTGT TATTACTCGC TGCCCAACCA GCCATGGCCG AGCTCGTGAT	6300
GACCCAGACT CCAGATATCC AACAGGAATG AGTGTTAATT CTAGAACCGG TCACTTGCCA	6360
CTGGCCGTGG TTTTACAACG TCGTGAAGTG GAAAACCCTG GCGTTACCCA AGCTTAATCG	6420
CCTTGAGAAA TTCCCTTTTG CCAGCTGGCG TAATAGCGAA GAGGCCCCGA CCGATCGCCC	6480
TTCCCAACAG TTGCGCAGCC TGAATGGCGA ATGGCGCTTT GCCTGGTTTC CGGCACCAGA	6540
AGCGGTGCCC GAAAGCTGGC TGGAGTGCGA TCTTCCTGAG GCCGATACGG TCCTCGTCCC	6600
CTCAAAGTGG CAGATGCACG GTTACGATGC GCCCATCTAC ACCAACGTAA CCTATCCCAT	6660
TACCGTCAAT CCGCCGTTTG TTCCACCGCA GAATCCGACG GGTGTTTACT CGCTCACATT	6720
TAATGTTGAT GAAAGCTGGC TACAGGAAGG CCAGACGCGA ATTATTTTGT ATGGCGTTCC	6780
TATTGGTTAA AAAATGAGCT GATTTAACAA AAATTTAACC CGAATTTTAA CAAAATATTA	6840

ACGTTTACAA TTTAAATATT TGCTTATACA ATCTTCCTGT TTTTGGGGCT TTTCTGATTA	6900
TCAACCGGGG TACATATGAT TGACATGCTA GTTTTACGAT TACCGTTCAT CGATTCTCTT	6960
GTTTGCTCCA GACTCTCAGG CAATGACCTG ATAGCCTTTG TAGATCTCTC AAAAATAGCT	7020
ACGCTCTCCG GCATTAAATTT ATCAGCTAGA ACGGTGGAAT ATCATATTGA TGGTGATTTG	7080
ACTGTCTCCG GCCTTTCTCA CCCTTTTGAA TCTTTACCTA CACATTACTC AGGCATTGCA	7140
TTTAAAATAT ATGAGGGTTC TAAAAATTTT TATCCTTGCG TTGAAATAAA GGCTTCTCCC	7200
GCAAAAGTAT TACAGGTCA TAATGTTTTT GGTACAACCG ATTTAGCTTT ATGCTCTGAG	7260
GCCTTATTGC TTAATTTTGC TAATTCCTTG CCTTGCTGT ATGATTTATT GGATGTT	7317

(2) INFORMATION FOR SEQ ID NO:3:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 7729 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: circular

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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CGTTCCGAGA ATTGGGAATC AACTGTTACA TGGAAATGAAA CTTCCAGACA CCGTACTTTA	180
GTTGCATATT TAAAACATGT TGAGCTACAG CACCAGATTC AGCAATTAAG CTCTAAGCCA	240
TCTGCAAAAA TGACCTCTTA TCAAAAGGAG CAATTAAAGG TACTCTCTAA TCCTGACCTG	300
TTGGAGTTTG CTTCGGTCT GGTTCGCTTT GAAGCTCGAA TTAAAACGCG ATATTGAAG	360
TCTTCGGGC TTCCTCTTAA TCTTTTIGAT GCAATCCGCT TTGCTTCTGA CTATAATAGT	420
CAGGGTAAAG ACCTGATTTT TGATTTATGG TCATTCTCGT TTTCTGAACT GTTTAAAGCA	480
TTTGAGGGGG ATTCAATGAA TATTTATGAC GATTCCGCAG TATTGGACGC TATCCAGTCT	540
AAACATTTTA CTATTACCCC CTCTGGCAA ACTTCTTTTG CAAAAGCCTC TCGCTATTTT	600
GGTTTTTATC GTCGTCTGGT AAACGAGGGT TATGATAGTG TTGCTCTTAC TATGCCTCGT	660
AATTCCTTTT GCGGTTATGT ATCTGCATTA GTTGAATGTG GTATTCCTAA ATCTCAACTG	720
ATGAATCTTT CTACCTGTAA TAATGTTGTT CCGTTAGTTC GTTTTATTAA CGTAGATTTT	780
TCTTCCCAAC GTCCTGACTG GTATAATGAG CCAGTTCTTA AAATCGCATA AGGTAATTCA	840
CAATGATTAA AGTTGAAATT AAACCATCTC AAGCCCAATT TACTACTCGT TCTGGTGTTT	900
GTCGTCAGGG CAAGCCTTAT TCACTGAATG AGCAGCTTTG TTACGTTGAT TTGGGTAATG	960
AATATCCGGT TCTTGTCAAG ATTACTCTTG ATGAAGGTCA GCCAGCCTAT GCGCCTGGTC	1020
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GTCTGCGCCT CGTTCGGGCT AAGTAACATG GAGCAGGTCC CGGATTTCCA CACAATTTAT	1140
CAGGCGATGA TACAAATCTC CGTTGTACTT TGTTTCGCGC TTGGTATAAT CGCTGGGGGT	1200

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GTGGCATTAC STATTTTACC CGTTTAATGG AAACTTCCTC ATGAAAAAGT CTTTAGTCCT	1320
CAAAGCCTCT GTAGCCGTTG CTACCCTCGT TCCGATGCTG TCTTTCGCTG CTGAGGGTGA	1380
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TGCGTGGGCG ATGGTTGTTG TCATTGTCCG CGCAACTATC GGTATCAAGC TGTTTAAGAA	1500
ATTCACCTCG AAAGCAAGCT GATAAACCGA TACAATTAAA GGCTCCTTTT GGAGCCTTTT	1560
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TTTACTAACC TCTGGAAGA CGACAAAAC TTAGATCGTT ACGCTAACTA TGAGGGTTGT	1740
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CAAGGCACTG ACCCCGTAA AACTTATTAC CAGTACACTC CTGTATCATC AAAAGCCATG	2160
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GATCCATTCTG TTTGTGAATA TCAAGGCCAA TCGTCTGACC TGCCTCAACC TCCTGTCAAT	2280
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GAAAACGGCG TACAGTCTGA CGCTAAAGGC AAACCTTGATT CTGTGCTAC TGATTACGGT	2520
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GGCTTAACTC AATTCTTGTG GGTATCTCT CTGATATTAG CGCTCAATTA CCCTCTGACT	3060
TTGTTCAAGG TGTTCACTTA ATTCTCCCGT CTAATGCGCT TCCCTGTTTT TATGTTATTC	3120
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CTTAGAATAC CSGATAAGCC TTCTATATCT GATTTCGCTG CTATTGGGCG CGGTAATGAT	3420
TCCTACGATG AAAATAAAAA CGGCTTGCTT GTTCTCGATG AGTGCGGTAC TTGGTTTAAT	3480
ACCCGTTCTT GGAATGATAA GGAAAGACAG CCGATTATTG ATTGGTTTCT ACATGCTCGT	3540
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ACTGGAAGA ATTTGTATAA CGCATATGAT ACTAAACAGG CTTTTCTAG TAATTATGAT	3840
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ACGACAGGTT TCCCGACTGG AAAGCGGGCA GTGAGCGCAA CGCAATTAAT GTGAGTTAGC	6120
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AAAAAATGAG CTGATTAAAC AAAAAATTTAA CGCGAATTTT AACAAAATAT TAACGTTTAC	7260
AATTTAAATA TTTGCTTATA CAATCTTCCT GTTTTTGGGG CTTTTCTGAT TATCAACCGG	7320

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CAGACTCTCA GGCAATGACC TGATAGCCTT TGTAGATCTC TCAAAAATAG CTACCCTCTC	7440
CGGCATTAAT TTATCAGCTA GAACGGTTGA ATATCATATT GATGGTGATT TGA CTGTCTC	7500
CGGCCTTTCT CACCCTTTTG AATCTTTACC TACACATTAC TCAGGCATTG CATTAAAAAT	7560
ATATGAGGGT TCTAAAAAT TTTATCCTTG CGTTGAAATA AAGGCTTCTC CCGCAAAAGT	7620
ATTACAGGGT CATAATGTTT TTGGTACAAC CGATTAGCT TTATGCTCTG AGGCTTTATT	7680
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(2) INFORMATION FOR SEQ ID NO:4:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7557 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: circular

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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GTTGCATATT TAAACATGT TGAGCTACAG CACCAGATTC AGCAATTAAG CTCTAAGCCA	240
TCCGCAAAAA TGACCTCTTA TCAAAAGGAG CAATTAAAGG TACTCTCTAA TCCTGACCTG	300
TTGGAGTTTG CTTCCGGTCT GGTTCCGCTT GAAGCTCGAA TTAAACCCCG ATATTTGAAG	360
TCTTTCGGGC TTCCTCTTAA TCTTTTTCAT GCAATCCGCT TTGCTTCTGA CTATAATAGT	420
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GGTTTTATC GTCGTCTGGT AAACGAGGGT TATGATAGTG TTGCTCTTAC TATGCCTCGT	660
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CGTGCTAATA ATTTTGATAT GGTGGTTTCA ATTCCTTCCA TAATTCAGAA GTATAATCCA	4500
AACAATCAGG ATTATATTGA TGAATTGCCA TCATCTGATA ATCAGGAATA TGATGATAAT	4560
TCCGCTCCTT CTGGTGGTTT CTTTGTTCGG CAAAATGATA ATGTTACTCA AACTTTTAAA	4620
ATTAATAAEC TTCGGGCAAA GGATTTAATA CGAGTTGTGG AATTGTTTGT AAAGTCTAAT	4680
ACTTCTAAAT CCTCAAATGT ATTATCTATT GACGGCTCTA ATCTATTAGT TGTTAGTGCA	4740
CCTAAAGATA TTTTAGATAA CCTTCCTCAA TTCCTTTCTA CTGTTGATTT GCCAACTGAC	4800
CAGATATTGA TTCAGGGTTT GATATTTGAG GTTCAGCAAG GTGATGCTTT AGATTTTICA	4860
TTTGCTGCTG GGTCTCAGCG TGGCACTGTT GCAGGCGGTG TTAATACTGA CCGCCTCACC	4920
TCTGTTTTAT CTTCTGCTGG TGGTTCGTTT GGTATTTTTA ATGGCGATGT TTTAGGGCTA	4980
TCAGTTCGCG CATTAAAGAC TAATAGCCAT TCAAAAATAT TGTCTGTGCC ACGTATTCTT	5040
ACGCTTTCAG GTCAGAAGGG TTCTATCTCT GTTGGCCAGA ATGTCCCTTT TATTACTGGT	5100
CGTGTGACTG GTGAATCTGC CAATGTAAAT AATCCATTTT AGACGATTGA GCGTCAAAAT	5160
GTAGGTATTT CCATGAGCGT TTTTCTGTTT GCAATGGCTG GCGGTAATAT TGTCTGGAT	5220
ATTACCAGCA AGGCCGATAG TTTGAGTTCT TCTACTCAGG CAAGTGATGT TATTACTAAT	5280
CAAAGAAGTA TTGCTACAAC GGTAAATTTT CGTGATGGAC AGACTCTTTT ACTCGGTGGC	5340

CTCACTGATT ATAAAAACAC TTCTCAAGAT TCTGGCGTAC CGTTCCTGTC TAAATCCCT	5400
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CTCGTCAAAG CAACCATAGT ACGCGCCCTG TAGCGGCGCA TTAAGCGCGG CGGGTGTGGT	5520
GGTTACGGCG ACGGTGACCG CTACACTTGC CAGCGCCCTA GCGCCCGCTC CTTTCGCTTT	5580
CTTCCCTTCC TTTCTCGCCA CGTTCGCGCG CTTTCCCGCT CAAGTCTAA ATCGGGGGCT	5640
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GTCCACGTTT TTTAATAGTG GACTCTTGTT CCAAACCTGGA ACAACACTCA ACCCTATCTC	5820
GGGCTATTCT TTTGATTAT AAGGGATTT GCCGATTTCT GAACCACCAT CAAACAGGAT	5880
TTTCGCCTGC TGGGGCAAAC CAGCGTGGAC CGCTTGCTGC AACTCTCTCA GGGCCAGGCG	5940
GTGAAGGGCA ATCAGCTGTT GCGCGTCTCG CTGGTGAAAA GAAAAACCAC CCTGGCGCCC	6000
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GCCGCTGGAT TGTTATTACT CGCTGCCCAA CCAGCCATGG CCGAGCTCTT CCGCCCATCT	6300
GATGAGCAGT TGAATCTGG AACTGCCTCT GTTGTGTGCC TGCTGAATAA CTTCTATCCC	6360
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AGTGTACAG AGCAGGACAG CAAGGACAGC ACCTACAGCC TCAGCAGCAC CCTGACGCTG	6480
AGCAAAGCAG ACTACGAGAA ACACAAAGTC TACGCCCTGG AAGTCACCCA TCAGGGCCTG	6540
AGCTCGCCCG TCACAAAGAG CTTCAACAGG GGAGAGTGTT CTAGAACCGG TCACCTGGCA	6600
CTGGCCGTCG TTTTACAACG TCGTGAAGTG GAAAACCCCTG GCGTTACCCA AGCTTAATCG	6660
CCTTGCAGAA TTCCCTTTTC CCAGCTGGCG TAATAGCGAA GAGGCCCGCA CCGATCGCCC	6720
TTCCCAACAG TTGGCGAGCC TGAATGGCGA ATGGCGCTTT GCCTGGTTTC CGGCACCAGA	6780
AGCGGTGCCC GAAAGCTGGC TGGAGTGCGA TCTTCCTGAG GCCGATACCG TCGTCTGCCC	6840
CTCAAACTGG CAGATGCACG GTTACGATGC GCCCATCTAC ACCAACGTAA CCTATCCCAT	6900
TACGGTCAAT CCGCCGTTTG TTCCACCGGA GAATCCGACG GGTTCCTTACT CGCTCAGATT	6960
TAATGTTGAT GAAAGCTGGC TACAGGAAGG CCAGACGCGA ATTATTTTTG ATGGCGTTCC	7020
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TCAACCGGGG TACATATGAT TGACATGCTA GTTTTACGAT TACCGTTCAT CGATTCTCTT	7200
GTTTGCTCCA GACTCTCAGG CAATGACCTG ATAGCCTTTG TAGATCTCTC AAAAATAGCT	7260
ACCTCTCCG GCATTAAATT ATCAGCTAGA ACGGTTGAAT ATCATATTGA TGGTGATTG	7320
ACTGTCTCCG GCCTTTCTCA CCCTTTTGAA TCTTTACCTA CACATTACTC AGGCATTGCA	7380

TTTAAATAT ATGAGGGTTC TAAAAATTTT TATCCTTGCG TTGAAATAAA GGCTTCTCCC 7440
 GCAAAAGTAT TACAGGGTCA TAATGTTTTT GGTACAACCG ATTTAGCTTT ATGCTCTGAG 7500
 GCTTTATTGC TTAATTTTGC TAATTCTTTG CCTTGCCTGT ATGATTTATT GGATGTT 7557

(2) INFORMATION FOR SEQ ID NO:5:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8118 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: circular

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AATGCTACTA CTATTAGTAG AATTGATGCC ACCTTTTCAG CTCGGGCCCC AAATGAAAAAT 60
 ATAGCTAAAC AGGTATTGA CCATTGCGA AATGTATCTA ATGGTCAAAC TAAATCTACT 120
 CGTTCCGAGA ATTGGGAATC AACTGTTACA TGGAAATGAAA CTTCCAGACA CCGTACTTTA 180
 GTTGCAATAT TAAACATGT TGAGCTACAG CACCAGATTC AGCAATTAAG CTCTAAGCCA 240
 TCTGCAAAAA TGACCTCTTA TCAAAAGGAG CAATTAAAGG TACTCTCTAA TCCTGACCTG 300
 TTGGAGTTTG CTTCGGTCT GGTTCGCTTT GAAGCTCGAA TTAAACGCG ATATTTGAAG 360
 TCTTCGGGGC TTCCTCTTAA TCTTTTIGAT GCAATCCGCT TTGCTTCTGA CTATAATAGT 420
 CAGGGTAAAG ACCTGATTTT TGATTTATGG TCATTCTCGT TTTCTGAACT GTTTAAAGCA 480
 TTTGAGGGGG ATTCAATGAA TATTTATGAC GATTCCGCAG TATTGGACGC TATCCAGTCT 540
 AAACATTTTA CTATTACCCC CTCTGGCAA ACTTCTTTTG CAAAAGCCTC TCGTATTTT 600
 GGTTTTTATC GTCGTCTGGT AAACGAGGGT TATGATAGTG TTGCTCTTAC TATGCCTCGT 660
 AATTCCTTTT GGCCTTATGT ATCTGCATTA GTTGAATGTG GTATTCCTAA ATCTCAACTG 720
 ATGAATCTTT CTACCTGTAA TAATGTTGTT CCGTTAGTTC GTTTTATTAA CGTAGATTTT 780
 TCTTCCCAAC³ GTCCTGACTG GTATAATGAG CCAGTCTTA AAATCGCATA AGGTAATTCA 840
 CAATGATTAA AGTTGAAATT AAACCATCTC AAGCCCAATT TACTACTCGT TCTGGTGTTT 900
 CTCGTCAGGG CAAGCCTTAT TCACTGAATG AGCAGCTTTG TIACGTTGAT TTGGGTAATG 960
 AATATCCGGT TCTTGCAAG ATTACTCTTG ATGAAGGTCA GCCAGCCTAT GCGCCTGGTC 1020
 TGTACACCGT TCATCTGTCC TCTTCAAAG TTGGTCAGTT CCGTTCCCTT ATGATTGACC 1080
 GTCTGCGCCT CGTTCCGGCT AAGTAACATG GAGCAGGTCTG CGGATTTCTGA CACAATTTAT 1140
 CAGGCGATGA TACAAATCTC CGTTGTACTT TGTTTCGCGC TTGGTATAAT CGCTGGGGGT 1200
 CAAAGATGAG TGTTTTAGTG TATTCCTTCG CCTCTTTCGT TTTAGGTTGG TGCCTTCGTA 1260
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 CAAAGCCTCT GTAGCCGTTG CTACCCTCGT TCCGATGCTG TCTTTCGCTG CTGAGGGTGA 1380
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TATTCTCACT CCGCTGAAAC TGTGAAAGT TGTITAGCAA AACCCCATAC AGAAAATTCA	1680
TTTACTAACG TCTGGAAAGA CGACAAAAC TTAGATCGTT ACGCTAACTA TGAGGGTTGT	1740
CTGTGGAATG CTACAGGCGT TGTAGTTTGT ACTGGTGACG AAACCTCAGTG TTACGGTACA	1800
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TCTGAGGGTG GCGGTCTGA GGGTGGCGGT ACTAAACCTC CTGAGTACGG TGATACACCT	1920
ATTCCGGGGCT ATACTTATAT CAACCCTCTC GACGGCACTT ATCCGCCTGG TACTGAGCAA	1980
AACCCCGCTA ATCCTAATCC TTCTCTTGAG GAGTCTCAGC CTCTTAATAC TTTCAITTTT	2040
CAGAATAATA GGTTCGGAAA TAGGCAGGGG GCATTAAC TG TTTATACGGG CACTGTACT	2100
CAAGGCACTG ACCCGGTAA AACTTATTAC CAGTACACTC CTGTATCATC AAAAGCCATG	2160
TATGACGCTT ACTGGAACGG TAAATTCAGA GACTGCGCTT TCCATTCTGG CTTTAATGAA	2220
GATCCATTCTG TTTGTGAATA TCAAGGCCAA TCGTCTGACC TGCCTCAACC TCCTGTCAAT	2280
GCTGGCGGGG GCTCTGGTGG TGGTCTGGT GCGGGCTCTG AGGGTGGTGG CTCTGAGGGT	2340
GGCGGTCTCTG AGGGTGGCGG CTCTGAGGGA GCGGGTTCCG GTGGTGGCTC TGGTTCGGGT	2400
GATTTTGATT ATGAAAAGAT GGCAAACGCT AATAAGGGGG CTATGACCGA AAATGCCGAT	2460
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GGTGATTTTG CTGGCTCTAA TTCCCAAATG GCTCAAGTCG GTGACGGTGA TAATTCACCT	2640
TTAATGAATA ATTTCCGTCA ATATTTACCT TCCCTCCCTC AATCGGTTGA ATGTGCGCCT	2700
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TTCCGTGGTG TCTTTGCGTT TCTTTTATAT GTTGCCACCT TTATGTATGT ATTTTCTACG	2820
TTTGCTAACA TACTGCGTAA TAAGGAGTCT TAATCATGCC AGTTCTTTTG GGTATTCCGT	2880
TATTATTGCG TTTCCTCGGT TTCCTTCTGG TAACTTTGTT CCGCTATCTG CTTACTTTTC	2940
TTAAAAAGGG GTTCGGTAAG ATAGCTATTG GTATTTCATT GTTCTTGCT CTTATTATTG	3000
GGCTTAACTC AATCTTGTG GGTATCTCT CTGATATTAG CGCTCAATTA CCCTCTGACT	3060
TTGTTCAGGG TGTTCACTTA ATTCTCCCGT CTAATGCGCT TCCGTGTTTT TATGTTATTC	3120
TCTCTGTAAA GGCTGCTATT TTCATTTTTG ACGTTAAACA AAAAATCGTT TCTTATTTGG	3180
ATTGGGATAA ATAATATGGC TGTITATTTT GTAACGGCA AATTAGGCTC TGGAAAGACG	3240
CTCGTTAGCG TTGGTAAGAT TCAGGATAAA ATTGTAGCTG GGTGCAAAAT AGCAACTAAT	3300
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TCCTACGATG AAAATAAAAA CGGCTTGCTT GTTCTCGATG AGTGCGGTAC TTGGTTTAAT	3480
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CCTCACCTCT GTTTTATCTT CTGCTGGTGG TTCGTTCCGT ATTTTAAATG GCGATGTTTT	4980
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GGCCGATACG GTCGTCGTCC CCTCAAACTG GCAGATGCAC GGTTACGATG CGCCCATCTA	7440
CACCAACGTA ACCTATCCCA TTACGGTCAA TCCGCCGTTT GTTCCCACGG AGAATCCGAC	7500
GGGTTGTTAC TCGCTCACAT TTAATGTTGA TGAAAGCTGG CTACAGGAAG GCCAGACGGC	7560
AATTATTTTT GATGGCGTTC CTATTGGTTA AAAAATGAGC TGATTTAACA AAAATTTAAC	7620

GCGAATTTTA ACAAATATT AACGTTTACA ATTTAAATAT TTGCTTATAC AATCTTCCTG	7680
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GATTTAGCTT TATGCTCTGA GGCTTTATTG CTTAATTTTG CTAATTCTTT GCCTTGCCTG	8100
TATGATTTAT TGGACGTT	8118

(2) INFORMATION FOR SEQ ID NO:6:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: misc_difference
- (B) LOCATION: replace(5, "")
- (D) OTHER INFORMATION: /note= "S REPRESENTS EQUAL MIXTURE OF G AND C"

(ix) FEATURE:

- (A) NAME/KEY: misc_difference
- (B) LOCATION: replace(6, "")
- (D) OTHER INFORMATION: /note= "M REPRESENTS EQUAL MIXTURE OF A AND C"

(ix) FEATURE:

- (A) NAME/KEY: misc_difference
- (B) LOCATION: replace(8, "")
- (D) OTHER INFORMATION: /note= "R REPRESENTS EQUAL MIXTURE OF A AND G"

(ix) FEATURE:

- (A) NAME/KEY: misc_difference
- (B) LOCATION: replace(11, "")
- (D) OTHER INFORMATION: /note= "K REPRESENTS EQUAL MIXTURE OF G AND T"

(ix) FEATURE:

- (A) NAME/KEY: misc_difference
- (B) LOCATION: replace(20, "")
- (D) OTHER INFORMATION: /note= "W REPRESENTS EQUAL MIXTURE OF A AND T"

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AGGTSMARCT KCTCCAGTCW GG

(2) INFORMATION FOR SEQ ID NO:7:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AGGTCCAGCT GCTCGAGTCT GG

22

(2) INFORMATION FOR SEQ ID NO:8:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AGGTCCAGCT GCTCGAGTCA GG

22

(2) INFORMATION FOR SEQ ID NO:9:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AGGTCCAGCT TCTCGAGTCT GG

22

(2) INFORMATION FOR SEQ ID NO:10:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AGGTCCAGCT TCTCGAGTCA GG

22

(2) INFORMATION FOR SEQ ID NO:11:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:11:
AGGTCCAACT GCTCGAGTCT GG

22

(2) INFORMATION FOR SEQ ID NO:12:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:12:
AGGTCCAACT GCTCGAGTCA GG

22

(2) INFORMATION FOR SEQ ID NO:13:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:13:
AGGTCCAACT TCTCGAGTCT GG

22

(2) INFORMATION FOR SEQ ID NO:14:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:14:
AGGTCCAACT TCTCGAGTCA GG

22

(2) INFORMATION FOR SEQ ID NO:15:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(1x) FEATURE:
 (A) NAME/KEY: misc_difference
 (B) LOCATION: replace(5..6, "")
 (D) OTHER INFORMATION: /note= "N-INOSINE"

(1x) FEATURE:
 (A) NAME/KEY: misc_difference
 (B) LOCATION: replace(8, "")
 (D) OTHER INFORMATION: /note= "N-INOSINE"

(1x) FEATURE:

- (A) NAME/KEY: misc_difference
- (B) LOCATION: replace(11, "")
- (D) OTHER INFORMATION: /note- "N-INOSINE"

(1x) FEATURE:

- (A) NAME/KEY: misc_difference
- (B) LOCATION: replace(20, "")
- (D) OTHER INFORMATION: /note- "W REPRESENTS EQUAL MIXTURE OF A AND T"

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AGGTNNANCT NCTCGAGTCW GG

22

(2) INFORMATION FOR SEQ ID NO:16:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CTATTAATA GTAACGGTAA CAGTGGTGCC TTGCCCCA

38

(2) INFORMATION FOR SEQ ID NO:17:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AGGCTTACTA GTACAATCCC TGGGCACAAT

30

(2) INFORMATION FOR SEQ ID NO:18:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCAGTTCGGA GCTCGTTGTG ACTCAGGAAT CT

32

(2) INFORMATION FOR SEQ ID NO:19:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CCAGTTCCGA GCTCGTGTTG ACCGAGCCGC CC

32

(2) INFORMATION FOR SEQ ID NO:20:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CCAGTTCCGA GCTCGTGCTC ACCCAGTCTC CA

32

(2) INFORMATION FOR SEQ ID NO:21:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CCAGTTCCGA GCTCCAGATG ACCCAGTCTC CA

32

(2) INFORMATION FOR SEQ ID NO:22:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CCAGATGTGA GCTCGTGATG ACCCAGACTC CA

32

(2) INFORMATION FOR SEQ ID NO:23:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CCAGATGTGA GCTCGTCATG ACCCAGTCTC CA

32

(2) INFORMATION FOR SEQ ID NO:24:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CCAGTTCCGA GCTCGTGATG ACACAGTCTC CA

32

(2) INFORMATION FOR SEQ ID NO:25:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GCAGCATTCT AGAGTTTCAG CTCCAGCTTG CC

32

(2) INFORMATION FOR SEQ ID NO:26:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GCGCCGTCTA GAATTAACAC TCATTCCTGT TGAA

34

(2) INFORMATION FOR SEQ ID NO:27:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1)³ SEQUENCE DESCRIPTION: SEQ ID NO:27:

GATCCTAGGC TGAAGGCGAT GACCCTGCTA AGGCTGC

37

(2) INFORMATION FOR SEQ ID NO:28:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:28:

ATTCAATAGT TTACAGGCAA GTGCTACTGA GTACA

35

(2) INFORMATION FOR SEQ ID NO:29:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TTGGCTACGC TTGGGCTATG GTAGTAGTTA TAGTT

35

(2) INFORMATION FOR SEQ ID NO:30:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GGTGCTACCA TAGGGATTAA ATTATTCAAA AAGTT

35

(2) INFORMATION FOR SEQ ID NO:31:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TACGAGCAAG GCTTCTTA

18

(2) INFORMATION FOR SEQ ID NO:32:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:32:

AGCTTAAGAA GCCTTGCTCG TAAACTTTTT GAATAATTT

39

(2) INFORMATION FOR SEQ ID NO:33:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:33:

AATCCCTATG GTAGCACCAA CTATAACTAC TACCAT

36

(2) INFORMATION FOR SEQ ID NO:34:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:34:

AGCCCAAGCG TAGCCAATGT ACTCAGTAGC ACTTC

35

(2) INFORMATION FOR SEQ ID NO:35:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CCTGTAAACT ATTGAATGCA GCCTTAGCAG GGTC

34

(2) INFORMATION FOR SEQ ID NO:36:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:36:

ATCGCCTTGA GCCTAG

16

(2) INFORMATION FOR SEQ ID NO:37:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CATTTTGGCA GATGGCTTAG A

21

(2) INFORMATION FOR SEQ ID NO:38:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TAGCATTAAAC GTCCAATA

18

(2) INFORMATION FOR SEQ ID NO:39:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:39:

ATATATTTTGA GTAAGCTTCA TCTTCT

26

(2) INFORMATION FOR SEQ ID NO:40:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GACAAAGAAC GCGTGAAAAC TTT

23

(2) INFORMATION FOR SEQ ID NO:41:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GCGGGCCTCT TCGCTATTGC TTAAGAAGCC TTGCT

35

(2) INFORMATION FOR SEQ ID NO:42:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:42:

AAACGACGGC CAGTGCCAAG TCACGGGTGT GAAATTGTGA TCC

43

(2) INFORMATION FOR SEQ ID NO:43:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GGCGAAAGGG AATTCTGCAA GGCGATTAAAG CTTGGGTAAC GCC

43

(2) INFORMATION FOR SEQ ID NO:44:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GGCGTTACCC AAGCTTTGTA CATGGAGAAA ATAAAG

36

(2) INFORMATION FOR SEQ ID NO:45:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 42 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TGAAACAAAG CACTATTGCA CTGGCACTCT TACCGTTACC GT

42

(2) INFORMATION FOR SEQ ID NO:46:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 42 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TACTGTTTAC CCCTGTGACA AAAGCCGCCC AGGTCCAGCT GC

42

(2) INFORMATION FOR SEQ ID NO:47:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 44 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:47:

TCGAGTCAGG CCTATTGTGC CCAGGGATTG TACTAGTGA TCCG

44

(2) INFORMATION FOR SEQ ID NO:48:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:48:

TGGCGAAAGG GAATTCGGAT CCACTAGTAC AATCCCTG

38

(2) INFORMATION FOR SEQ ID NO:49:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GGCACAATAG GCCTGACTCG AGCAGCTGGA CCAGGGCGGC TT

42

(2) INFORMATION FOR SEQ ID NO:50:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:50:

TTGTCACAGG GGTAAACAGT AACGGTAACG GTAAGTGTCC CA

42

(2) INFORMATION FOR SEQ ID NO:51:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GTGCAATAGT GCTTTGTTTC ACTTTATTTT CTCCATGTAC AA

42

(2) INFORMATION FOR SEQ ID NO:52:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:52:
TAACGGTAAG AGTGCCAGTG C

21

(2) INFORMATION FOR SEQ ID NO:53:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:53:
CACCTTCATG AATTCGGCAA GGAGACAGTC AT

32

(2) INFORMATION FOR SEQ ID NO:54:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:54:
AATTCGCCAA GGAGACAGTC AT

22

(2) INFORMATION FOR SEQ ID NO:55:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:55:
AATGAAATAC CTATTGCCTA CGGCAGCCGC TGGATTGTT

39

(2) INFORMATION FOR SEQ ID NO:56:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:56:
ATTACTCGCT GCCCAACCAG CCATGCCCGA GCTCGTGAT

39

(2) INFORMATION FOR SEQ ID NO:57:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GACCCAGACT CCAGATATCC AACAGGAATC AGTGTTAAT

39

(2) INFORMATION FOR SEQ ID NO:58:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:58:

TCTAGAACGC GTC

13

(2) INFORMATION FOR SEQ ID NO:59:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:59:

TTCAGGTTGA AGCTTACGGC TTCTAGAATT AACACTCATT CCTGT

45

(2) INFORMATION FOR SEQ ID NO:60:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:60:

TGGATATCTG GAGTCTGGGT CATCAGGAGC TCGGCCATG

39

(2) INFORMATION FOR SEQ ID NO:61:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GCTGGTTGGG CAGCGAGTAA TAACAATCCA GCGGCTGCC

39

(2) INFORMATION FOR SEQ ID NO:62:

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GTAGGCAATA GGTATTTTCAT TATGACTGTC CTTGGCG

37

(2) INFORMATION FOR SEQ ID NO:63:

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:63:

TGACTGTCTC CTTGGCGTGT GAAATGTGA

30

(2) INFORMATION FOR SEQ ID NO:64:

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:64:

TAACACTCAT TCCGGATGGA ATTCTGGAGT CTGGGT

36

(2) INFORMATION FOR SEQ ID NO:65:

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GCCAGTGCCA AGTGACGCGT TCTA

24

(2) INFORMATION FOR SEQ ID NO:66:

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:66:

ATATATTTTA GTAAGCTTCA TCTTCT

(2) INFORMATION FOR SEQ ID NO:67:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

26

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GACAAAGAAC GCGTGAAAAC TTT

(2) INFORMATION FOR SEQ ID NO:68:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 76 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

23

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:68:

CTGAACCTGT CTGGGACCAC AGTTGATGCT ATAGGATCAG ATCTAGAATT CATTAGAGA
CTGGCCTGGC TTCTGC

60

(2) INFORMATION FOR SEQ ID NO:69:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 80 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

76

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:69:

TCGACCGTTG GTAGGAATAA TGCAATTAAAT GGAGTAGCTC TAAATTCAGA ATTCATCTAC
ACCCAGTGCA TCCAGTAGCT

60

(2) INFORMATION FOR SEQ ID NO:70:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

80

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GGTAAACAGT AACGGTAAGA GTGCCAG

27

(2) INFORMATION FOR SEQ ID NO:71:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:71:

CGCCTTCAGC CTAAGAAGCG TAGTCCGGAA CGTCGTACGG GTAGGATCCA CTAG

54

(2) INFORMATION FOR SEQ ID NO:72:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:72:

CACCGGTTCC GGAATTAGT CTGACCAGG CAGCCCAGGG C

41

(2) INFORMATION FOR SEQ ID NO:73:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:73:

ATTCCACACA TTATACGAGC CGGAAGCATA AAGTGTCAG CCTGGGGTGC C

51

(2) INFORMATION FOR SEQ ID NO:74:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 42 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:74:

CTGCTCATCA GATGGCGGGA AGAGCTCGGC CATGGCTGGT TG

42

(2) INFORMATION FOR SEQ ID NO:75:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 42 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

78

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:75:

GAACAGAGTG ACCGAGGGGG CGAGCTCGGC CATGGCTGGT TG

42